

PATENT
USSN 08/974,584
015389-002950US
018/206p2

APPENDIX A**BEST AVAILABLE COPY****Mouse TERT protein sequence**

LOCUS 070372 1122 aa linear ROD 15-JUN-2002
DEFINITION Telomerase reverse transcriptase (Telomerase catalytic subunit).
ORGANISM Mus musculus
AUTHORS Greenberg,R.A., Allsopp,R.C., Chin,L., Morin,G.B. and DePinho,R.A.
TITLE Expression of mouse telomerase reverse transcriptase during
development, differentiation and proliferation
JOURNAL Oncogene 16 (13), 1723-1730 (1998)

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1 mtraprcpav rsllrsryre vwplatfvrr lgpegrrlvq pgdpkiyrtl vaqclvcmh  
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121 sylvntviet lrvsgawmll lsrvgddlly yllahcalyl lvppscayqv cgsplyqica  
181 ttidiwpsvsa syrptrpvgr nftnlrflqq iksssrqcap kplalpsrgt krhlsltsts  
241 vpsakkarcy pvprveegph rqvltptsgk swvpsparsp evptaekdls skgkvsdls  
301 sgsvcckhkp sstslsppr qnafqlrpfi etrhflysrg dgqerlnpsf llsnlqpnlt  
361 garrlveiif lgsrprtsqp lcrthrlsrr ywqmrplfqf llvnhacqy vrlrshcrf  
421 rtanqqvtda lntspplmd lirlhsspwq vygfllracf kvvsaslwgt rhnerrffkn  
481 lkkfislgyk gklslqelmw kmkvedchw l rsspdkdrvp aaehrlreri latflfwlmd  
541 tyvvqlrsf fyitestfqq nrlffyrksv wsklqsigvr qhlervrlre lsqeevrhhq  
601 dtwlampicr lrfipkpngl rpivnmsysm gtralgrrkq aqhftqrlkt lfsmlnyert  
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SEQ. ID NO:124 (Figure 60)

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CAGTCTGTGT TTCGAGACA TGGAGAACA GCTGTTTGCT GAGGTGACG GGGATGGGT 2640
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ORF Finder (Open Reading Frame Finder)

PubMed

Entrez

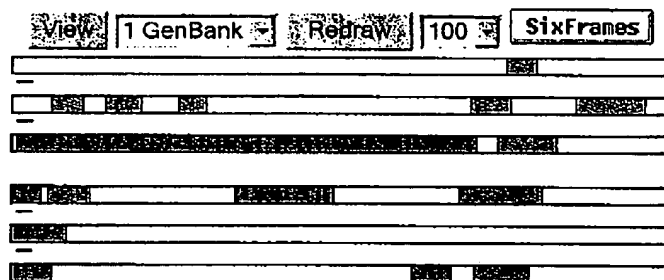
BLAST

OMIM

Taxonomy

Structure

Anonymous

Program ☒ blastp Database ☐ nr ☒ BLAST ☐ with parameters ☒ Cognitor

Length: 702 aa

View: ☒ GenBank ☐ Redraw ☐ 100 ☒ SixFrames

Frame from to Length

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-1	1040..1486	447
-1	2060..2443	384
+2	2600..2917	318
+3	2241..2510	270
-3	2127..2387	261
-2	1..258	258
-1	170..370	201
-3	1..191	191
+2	2117..2302	186
-3	1842..2018	177
+2	440..604	165
+2	191..337	147
-1	2..139	138
+1	2281..2415	135
+2	776..907	132

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123 ctggggcccgaggcaggcggctgtgcaacccggggaccogaag
L G P E G R R L V Q P G D P K
168 atctaccgcactttggttgcccaatgcctagtgtgcactgcactgg
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213 ggctcacagcctccacctgcccagcctttccttcaccaggtgtca
G S Q P P P A D L S F H Q V S
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S L K E L V A R V V Q R L C E
303 cgcaacgagagaaaacgtgctggttttggctttgagctgcttaac
R N E R N V L A F G F E L L N
348 gaggccagaggcgggctcccatggccttcactagtagcgtgcgt
E A R G G P P M A F T S S V R
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438 gcatggatgctactgttgagccgagtgggcgacgacctgctggtc
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528 tgtgacctaccaggtgtgtgggtctcccctgtaccaaatttgtgcc
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843 tcatgggtgccaagtccctgctcgggtcccccaggtgctactgca
S W V P S P A R S P E V P T A
888 gagaaagatttgtcttcttaaaggaaaggtgtctgacctgagttct
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933 tctgggtcgggtgtgctgtaaacacaagcccagctccacatctctg
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1023 gagaccagacatttccctttactccaggggagatggccaagagcgt
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1068 ctaaacccctcattcctactcagcaacctccagcctaacttgact
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1968 cagcgtctcaagactcttccagcatgctcaactatgagccgaca
Q R L K T L F S M L N Y E P T
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K H P H L M G S S V L G M N D
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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

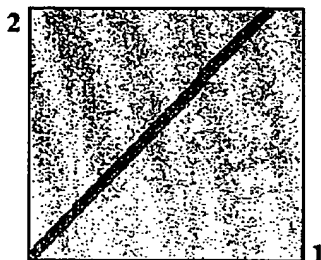
Structure

BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.13 [Nov-27-2005]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ View option **Standard**
Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Aug**

Sequence 1: lcl|seq_1
Length = 1122 (1 .. 1122)

Sequence 2: lcl|seq_2
Length = 3025 (1 .. 3025)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1595 bits (4129), Expect = 0.0
Identities = 830/1001 (82%), Positives = 840/1001 (83%), Gaps = 22/1001 (2%)
Frame = +3

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Sbjct	33	MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW	212
Query	61	GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120
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Query	121	SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA	180
Sbjct	393	SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA	572
Query	181	TTDIWPSVSASYRPTRPVGRNFTNLRFLQIQKSSSRQEAPKPLALPSRGTKRHLSTSTS	240
		TTDIWPSVSASYRPTRPVGRNFTNLRFLQIQKSSSRQEAPKPLALPSRGTKRHLSTSTS	

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Sbjct 753 VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVSPARSPEVPTAEKDLSSKGKVSDDL 932

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Sbjct 1113 GARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLRSHCRF 1292

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RTANQQVTDALNTSPPHMLDLLRLHSSPWQVYGLRACLCKVVSASLWGTRHNERRFFKN

Sbjct 1293 RTANQQVTDALNTSPPHMLDLLRLHSSPWQVYGLRACLCKVVSASLWGTRHNERRFFKN 1472

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+ S + CS + ++ G+ +V L K

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CPU time: 0.10 user secs. 0.00 sys. secs 0.10 total secs.

Lambda K H
0.325 0.137 0.426

PATENT
USSN 08/974,584
015389-002950US
018/206p2

T motif encoded in SEQ. ID NO:124 mTRT fragment

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mTERT:	61	GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120
SEQ. 124:	213	GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	392
mTERT:	121	SYLPNTVIETLRVSGAWMLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVC6SPLYQICA	180
SEQ. 124:	393	SYLPNTVIETLRVSGAWMLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVC6SPLYQICA	572
mTERT:	181	TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS	240
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SEQ. 124:	753	VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSNVPSPARSPEVPTAEKDLSSKGKVS DLSL	932
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SEQ. 124:	933	SGSVCCCKHKPSSTSLSPPRQNAFQLRPFIEIETHFLYSRGDGGQERLNPSFLLSNLQPNLT	1112
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SEQ. 124:	1113	GARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSHCRF	1292
mTERT:	421	RTANQQVTDALNTSPPHMDLLRLHSSPWQVYGFRLACLCKVVSASLWGTRHNERRFFKN	480
SEQ. 124:	1293	RTANQQVTDALNTSPPHMDLLRLHSSPWQVYGFRLACLCKVVSASLWGTRHNERRFFKN	1472
mTERT:	481	LKKFISLGKYGKLSLQELMWKMKVEDCHWLRS SPGKDRVPAAEHRLRERILATFLFWEND	540
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mTERT:	541	TYVVQLLRSEFFYITESTFOKNRLEFFYRKSVWSKLOSIGVROHLERVRLRELSQEEVRHHQ	600
SEQ. 124:	1653	TYVVQLLRSEFFYITESTFOKNRLEFFYRKSVWSKLOSIGVROHLERVRLRELSQEEVRHHQ	1832
mTERT:	601	DTWLAMPICRLRFIPKPNGLRPVNMSSYMGTRALGRRKQAQHTQRLKTLFSMLNYERT	660
SEQ. 124:	1833	DTWLAMPICRLRFIPKPNGLRPVNMSSYMGTRALGRRKQAQHTQRLKTLFSMLNYE T	2012
mTERT:	661	KPHLMGSSVLGMNDIYRTWRAFLVRALD	691
SEQ. 124:	2013	KPHLMGSSVLGMNDIYRTWRAFLVRALD	

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